SEQUENCE LISTING

<110> OLSON, ERIC
FREY, NORBERT

<120> METHODS AND COMPOSITIONS RELATING TO MUSCLE SPECIFIC
CALCINEURIN ASSOCIATED PROTEIN (CAP)

<130> UTSD:729US

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<141> 2001-11-07

<150> 60/246,629
<151> 2000-11-07

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<170> PatentIn Ver. 2.1

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Gln Leu Gly Thr Ala Gly Gln Gly Phe Ser Tyr Ser Lys Ser Asn Gly
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145                 150                 155                 160

Pro Lys Gly Tyr Arg Cys Pro Trp Gln Glu Phe Val Ser Tyr Arg Asp
                165                 170                 175

Tyr Gln Ser Asp Gly Arg Ser His Thr Pro Ser Pro Asn Asp Tyr Arg
            180                 185                 190

Asn Phe Asn Lys Thr Pro Val Pro Phe Gly Gly Pro Leu Val Gly Gly
        195                 200                 205

Thr Phe Pro Arg Pro Gly Thr Pro Phe Ile Pro Glu Pro Leu Ser Gly
    210                 215                 220

Leu Glu Leu Leu Arg Leu Arg Pro Ser Phe Asn Arg Val Ala Gln Gly
225                 230                 235                 240

Trp Val Arg Asn Leu Pro Glu Ser Glu Glu Leu
                245                 250


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<213> Mus musculus

<400> 11
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ttgggggtct gacatttctt cccatctact gtggccccac caggatgatc cccaaggagc 120
agaaggagcc agtgatggct gtcccggggg accttgctga accagtccct tcgctggacc 180
tggggaagaa gctgagcgtg cctcaggacc taatgataga ggagctgtct ctacgaaaca 240
accgcggatc cctcctcttt cagaagaggc agcgccgggt gcagaagttt acctttgagc 300
tatcagaaag tttgcaggcc atcctggcga gtagtgcccg agggaaagtg gctggcagag 360
```

```
cggcgcaggc aacggttccc aatggcttgg aggagcagaa ccaccactcc gagacgcacg 420
tgttccaggg gtcacctggg gaccccggga tcacccatct gggagcagcg gggactgggt 480
cggtccgtag tccaagcgcc ctggcaccag gctatgcaga gcccctgaag ggcgtcccac 540
cggagaagtt caaccacact gccatcccca aaggctaccg gtgcccttgg caggagttca 600
ccagctacca agactactcg agtggcagca gaagtcacac tcccatcccc cgagactatc 660
gcaacttcaa caagaccccc gtgccatttg gaggacccca cgtgagggag gccattttcc 720
acgcaggcac cccctttgtc ccggagtcct tcagtggctt ggaacttctc cgcctcagac 780
ccaatttcaa cagggttgct cagggctggg tccggaagct cccggagtct gaggaactgt 840
agcctcagcc tgaagctaca attccctggg ctcaagaaac atgcttgtct tgaaaaaaaa 900
aaaaaaaaaa aaa                                                    913


<210> 12
<211> 245
<212> PRT
<213> Mus musculus

<400> 12
Met Ile Pro Lys Glu Gln Lys Glu Pro Val Met Ala Val Pro Gly Asp
 1               5                  10                  15

Leu Ala Glu Pro Val Pro Ser Leu Asp Leu Gly Lys Lys Leu Ser Val
            20                  25                  30

Pro Gln Asp Leu Met Ile Glu Glu Leu Ser Leu Arg Asn Asn Arg Gly
        35                  40                  45

Ser Leu Leu Phe Gln Lys Arg Gln Arg Arg Val Gln Lys Phe Thr Phe
    50                  55                  60

Glu Leu Ser Glu Ser Leu Gln Ala Ile Leu Ala Ser Ser Ala Arg Gly
65                  70                  75                  80

Lys Val Ala Gly Arg Ala Ala Gln Ala Thr Val Pro Asn Gly Leu Glu
                85                  90                  95

Glu Gln Asn His His Ser Glu Thr His Val Phe Gln Gly Ser Pro Gly
            100                 105                 110

Asp Pro Gly Ile Thr His Leu Gly Ala Ala Gly Thr Gly Ser Val Arg
        115                 120                 125

Ser Pro Ser Ala Leu Ala Pro Gly Tyr Ala Glu Pro Leu Lys Gly Val
    130                 135                 140

Pro Pro Glu Lys Phe Asn His Thr Ala Ile Pro Lys Gly Tyr Arg Cys
145                 150                 155                 160

Pro Trp Gln Glu Phe Thr Ser Tyr Gln Asp Tyr Ser Ser Gly Ser Arg
                165                 170                 175

Ser His Thr Pro Ile Pro Arg Asp Tyr Arg Asn Phe Asn Lys Thr Pro
            180                 185                 190
```

```
Val Pro Phe Gly Gly Pro His Val Arg Glu Ala Ile Phe His Ala Gly
        195                 200                 205

Thr Pro Phe Val Pro Glu Ser Phe Ser Gly Leu Glu Leu Leu Arg Leu
    210                 215                 220

Arg Pro Asn Phe Asn Arg Val Ala Gln Gly Trp Val Arg Lys Leu Pro
225                 230                 235                 240

Glu Ser Glu Glu Leu
                245
```

human CAP-1

```
                                                           60
MLSHNTMMKQRKQQATAIMKEVHGNDVDGMDLGKKVSIPRDIMLEELSHLSNRGARLFKM

                                                          120
RQRRSDKYTFENFQYQSRAQINHSIAMQNGKVDGSNLEGGSQQAPLTPPNTPDPRSPPNP

                                                          180
DNIAPGYSGPLKEIPPEKFNTTAVPKYYQSPWEQAISNDPELLEALYPKLFKPEGKAELP

                                                          240
DYRSFNRVATPFGGFEKASRMVKFKVPDFELLLLTDPRFMSFVNPLSGRRSFNRTPKGWI

SENIPIVITTEPTDDTTVPESEDL
```

FIG. 1A

mouse CAP-1

```
                                                           60
MLSHSAMVKQRKQQASAITKEIHGHDVDGMDLGKKVSIPRDIMIEELSHFSNRGARLFKM

                                                          120
RQRRSDKYTFENFQYESRAQINHNIAMQNGRVDGSNLEGGSQQGPSTPPNTPDPRSPPNP

                                                          180
ENIAPGYSGPLKEIPPERFNTTAVPKYYRSPWEQAIGSDPELLEALYPKLFKPEGKAELR

                                                          240
DYRSFNRVATPFGGFEKASKMVKFKVPDFELLLLTDPRFLAFANPLSGRRCFNRAPKGWV

SENIPVVITTEPTEDATVPESDDL
```

FIG. 1B

human CAP-2

60
MPLSGTPAPNKKRKSSKLIMELTGGGQESSGLNLGKKISVPRDVMLEELSLLTNRGSKMF

120
KLRQMRVEKFIYENHPDVFSDSSMDHFQKFLPTVGGQLGTAGQGFSYSKSNGRGGSQAGG

180
SGSAGQYGSDQQHHLGSGSGAGGTGGPAGQAGRGGAAGTAGVGETGSGDQAGGEGKHITV

240
FKTYISPWERAMGVDPQQKMELGIDLLAYGAKAELPKYKSFNRTAMPYGGYEKASKRMTF

QMPKFDLGPLLSEPLVLYNQNLSNRPSFNRTPIPWLSSGEPVDYNVDIGIPLDGETEEL

FIG. 1C

mouse CAP-2

60
MPLSGTPAPNKRRKSSKLIMELTGGGRESSGLNLGKKISVPRDVMLEELSLLTNRGSKMF

120
KLRQMRVEKFIYENHPDVFSDSSMDHFQKFLPTVGGQLETAGQGFSYGKGSSGGQAGSSG

180
SAGQYGSDRHQQGSGFGAGGSGGPGGQAGGGGAPGTVGLGEPGSGDQAGGDGKHVTVFKT

240
YISPWDRAMGVDPQQKVELGIDLLAYGAKAELPKYKSFNRTAMPYGGYEKASKRMTFQMP

KFDLGPLLSEPLVLYNQNLSNRPSFNRTPIPWLSSGEHVDYNVDVGIPLDGETEEL

FIG. 1D

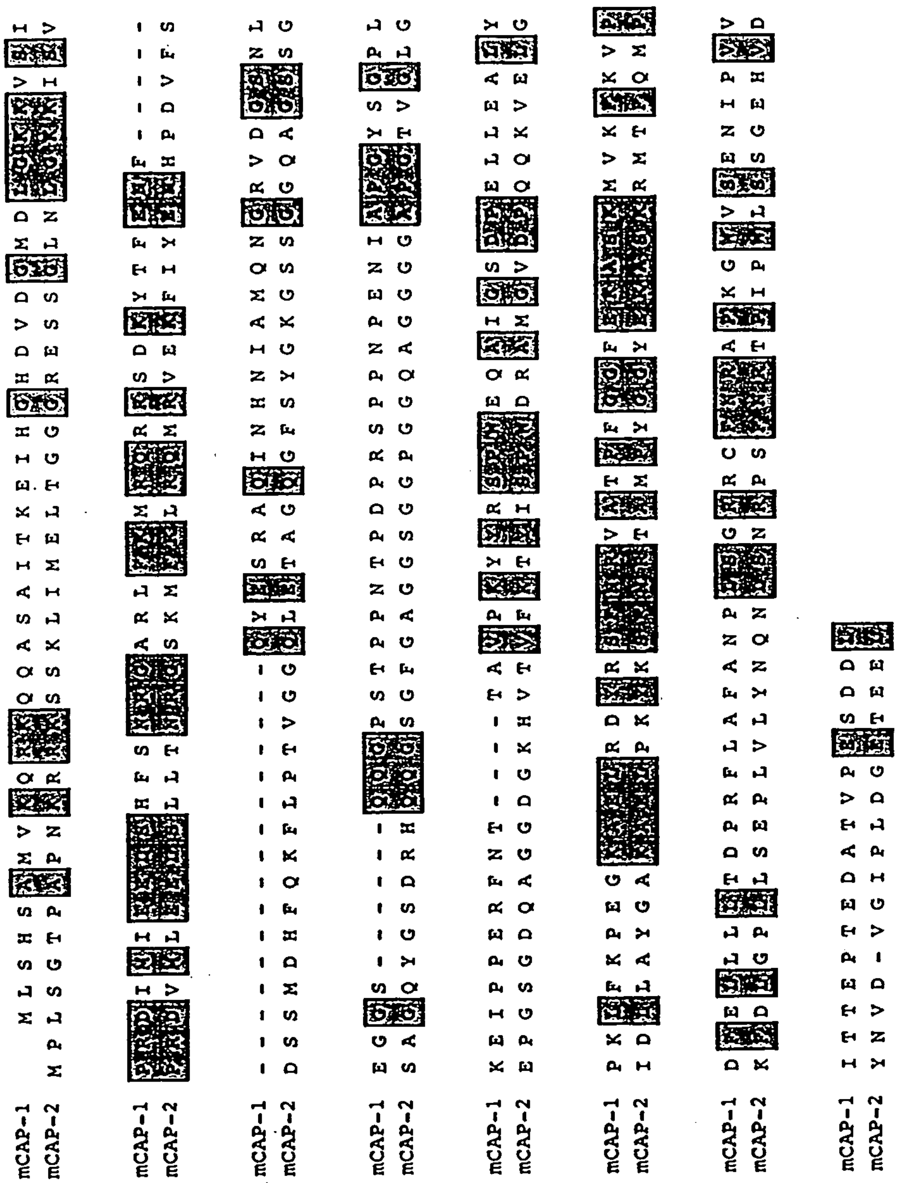


FIG. 1E

human CAP-1

```
       10        20        30        40        50        60        70        80        90       100
GTCCCAGGTTCAAGGATAAAAACCATCAGGCCCAAGTGCCATCCATAGTCCATCTCCAGAGTCTTCCTCCACAAACTGGGATTCATCCCCGCTGAAAAAG
CAGGGTCCAAGTTCCTATTTTTGGTAGTCCGGGTTCACGGTAGGTATCAGGTAGAGGTCTCAGAAGGAGGTGTTTGACCCTAAGTAGGGGCGACTTTTTC

      110       120       130       140       150       160       170       180       190       200
CACAATCTAACAGCAAGGGAACAAAAAAACCATGCTATCACATAATACTATGATGAAGCAGAGAAAACAGCAAGCAACAGCCATCATGAAGGAAGTCCAT
GTGTTAGATTGTCGTTCCCTTGTTTTTTTGGTACGATAGTGTATTATGATACTACTTCGTCTCTTTTGTCGTTCGTTGTCGGTAGTACTTCCTTCAGGTA

      210       220       230       240       250       260       270       280       290       300
GGAAATGATGTTGATGGCATGGACCTGGGCAAAAAGGTCAGCATCCCCAGAGACATCATGTTGGAAGAATTATCCCATCTCAGTAACCGTGGTGCCAGGC
CCTTTACTACAACTACCGTACCTGGACCCGTTTTTCCAGTCGTAGGGGTCTCTGTAGTACAACCTTCTTAATAGGGTAGAGTCATTGGCACCACGGTCCG

      310       320       330       340       350       360       370       380       390       400
TATTTAAGATGCGTCAAAGAAGATCTGACAAATACACATTTGAAAATTTCCAGTATCAATCTAGAGCACAAATAAATCACAGTATTGCTATGCAGAATGG
ATAAATTCTACGCAGTTTCTTCTAGACTGTTTATGTGTAAACTTTTAAAGGTCATAGTTAGATCTCGTGTTTATTTAGTGTCATAACGATACGTCTTACC

      410       420       430       440       450       460       470       480       490       500
GAAAGTGGATGGAAGTAACTTGGAAGGTGGTTCGCAGCAAGCCCCCTTGACTCCTCCCAACACCCCAGATCCACGAAGCCCTCCAAATCCAGACAACATT
CTTTCACCTACCTTCATTGAACCTTCCACCAAGCGTCGTTCGGGGGAACTGAGGAGGGTTGTGGGGTCTAGGTGCTTCGGGAGGTTTAGGTCTGTTGTAA

      510       520       530       540       550       560       570       580       590       600
GCTCCAGGATATTCTGGACCACTGAAGGAAATTCCTCCTGAAAAATTCAACACCACAGCTGTCCCTAAGTACTATCAATCTCCCTGGGAGCAAGCCATTA
CGAGGTCCTATAAGACCTGGTGACTTCCTTTAAGGAGGACTTTTTAAGTTGTGGTGTCGACAGGGATTCATGATAGTTAGAGGGACCCTCGTTCGGTAAT

      610       620       630       640       650       660       670       680       690       700
GCAATGATCCGGAGCTTTTAGAGGCTTTATATCCTAAACTTTTCAAGCCTGAAGGAAAGGCAGAACTGCCTGATTACAGGAGCTTTAACAGGGTTGCCAC
CGTTACTAGGCCTCGAAAATCTCCGAAATATAGGATTTGAAAAGTTCGGACTTCCTTTCCGTCTTGACGGACTAATGTCCTCGAAATTGTCCCAACGGTG

      710       720       730       740       750       760       770       780       790       800
ACCATTTGGAGGTTTTGAAAAAGCATCAAGAATGGTTAAATTTAAAGTTCCAGATTTTGAGCTACTATTGCTAACAGATCCCAGGTTTATGTCCTTTGTC
TGGTAAACCTCCAAAACTTTTTCGTAGTTCTTACCAATTTAAATTTCAAGGTCTAAAACTCGATGATAACGATTGTCTAGGGTCCAAATACAGGAAACAG

      810       820       830       840       850       860       870       880       890       900
AATCCCCTTTCTGGCAGACGGTCCTTTAATAGGACTCCTAAGGGATGGATATCTGAGAATATTCCTATAGTGATAACAACCGAACCTACAGATGATACCA
TTAGGGGAAAGACCGTCTGCCAGGAAATTATCCTGAGGATTCCCTACCTATAGACTCTTATAAGGATATCACTATTGTTGGCTTGGATGTCTACTATGGT

      910       920       930       940       950       960       970       980       990      1000
CTGTACCAGAATCAGAAGACCTATGAAAAGAAAGTTGTATGTGCCACATAAAACTCTGAATATAAAAGTTGCTGTTCTACTATTTTAACTACTGGCAAAG
GACATGGTCTTAGTCTTCTGGATACTTTTCTTTCAACATACACGGTGTATTTTGAGACTTATATTTTCAACGACAAGATGATAAAATTGATGACCGTTTC

     1010      1020      1030      1040      1050      1060      1070      1080      1090      1100
CACTTGCATTTTTCATTAGTAGCAACAATAGCAATTTAGTGATTTTCCTTTTCTGACATTCAATTTCAATCTCAGATCAAATACTAATAAACAATTAGAA
GTGAACGTAAAAAGTAATCATCGTTGTTATCGTTAAATCACTAAAAGGAAAAGACTGTAAGTTAAAGTTAGAGTCTAGTTTATGATTATTTGTTAATCTT

     1110      1120      1130      1140      1150      1160      1170      1180      1190      1200
ATCTTACTTTAAAAAACTTATAACTCACTTGTCTTCATTCATAATTTTGTTTTCACCTGGTTTAAAGAATCCAGATATTTTACTGCAAAAGTTCAGATGG
TAGAATGAAATTTTTTGAATATTGAGTGAACAGAAGTAAGTATTAAAACAAAAGTGGACCAAATTTCTTAGGTCTATAAAATGACGTTTTCAAGTCTACC

     1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
AAAAGTAATTGACAGCTTCACCTTTGTCTCATTTTATATGATTTATTACAGTGTAAGTTTTTCAAGTGGAATCTAGAATCAAAATACAGGGAGAGATATG
TTTTCATTAACTGTCGAAGTGGAAACAGAGTAAAATATACTAAATAATGTCACATTCAAAAAGTTCACCTTAGATCTTAGTTTTATGTCCCTCTCTATAC

     1310      1320      1330      1340      1350      1360      1370      1380      1390      1400
AAGACCTATTCAGAGTTTCATCTGGGGATGAAAGCTATGGAAGATGATGTACAAATGTTATTGATGGAGAAAATGGTTGGTGTGTCCTTTCTGGTGACCA
TTCTGGATAAGTCTCAAAGTAGACCCCTACTTTCGATACCTTCTACTACATGTTTACAATAACTACCTCTTTTACCAACCACACAGGAAAGACCACTGGT

     1410      1420      1430      1440      1450      1460      1470      1480      1490      1500
TGAGAAAATAATATGTCTTGATGAAGTCTTTTCATTAGTCACTCTTAGAATTCTAAAGTGCTTTGCACTTTTCAATATGTTTTGAATCATTAGGTAATTT
ACTCTTTTATTATACAGAACTACTTCAGAAAAGTAATCAGTGAGAATCTTAAGATTTCACGAAACGTGAAAAGTTATACAAAACTTAGTAATCCATTAAA

     1510      1520      1530      1540      1550      1560      1570      1580      1590      1600
ATTCTGGATGATATTCTCCAAAATTCAATTCAGTTATTATATTCATTTAGCATTAAGTCAAGGAGACTGAGAATGACTCAAGGGACGTCATAGTACCATA
TAAGACCTACTATAAGAGGTTTTAAGTTAAGTCAATAATATAAGTAAATCGTAATTCAGTTCCTCTGACTCTTACTGAGTTCCCTGCAGTATCATGGTAT

     1610      1620      1630      1640      1650      1660      1670      1680      1690      1700
GTTTTAAGGACCAAGGTGTGCCCAGAATTCAAGTTTCACAAATCCCAATGCTGTGCATTGATTATGTTCAACTTTATGTGTGCATTCTTAGAAGAGTAAG
CAAAATTCCTGGTTCCACACGGGTCTTAAGTTCAAAGTGTTTAGGGTTACGACACGTAACTAATACAAGTTGAAATACACACGTAAGAATCTTCTCATTC

     1710      1720      1730      1740      1750      1760      1770      1780      1790      1800
AACAAATAAAGTACACCGTAATATACATATAAATACATTCATGTTTGTGAGAGAAGGAAAGAGTAAGTAATTTGAATTGGCAGCTTTCTTTGCTAAATCT
TTGTTTATTTCATGTGGCATTATATGTATATTTATGTAAGTACAAACACTCTCTTCCTTTCTCATTCATTAAACTTAACCGTCGAAAGAAACGATTTAGA

     1810      1820      1830      1840      1850      1860      1870      1880      1890      1900
TTAAATTCTGTTAAGATCCTCAAGTAACTGGGGAGTACATGCTTTAGGACACAAACAAAAACAAAGGGCATGAAAGTATCTGAAAGCAATGTAGCACATA
AATTTAAGACAATTCTAGGAGTTCATTGACCCCTCATGTACGAAATCCTGTGTTTGTTTTTGTTTCCCGTACTTTCATAGACTTTCGTTACATCGTGTAT

     1910      1920      1930      1940      1950      1960      1970      1980      1990      2000
TCTATCGTAATATATGTAATATATTGACATAAAAGACACAAACTAATATAAAGTTATAGTTATATCTTAAAATATAATTGAAGAAGCATATGACATATAA
AGATAGCATTATATACATTATATAACTGTATTTTCTGTGTTTGATTATATTTCAATATCAATATAGAATTTTATATTAACTTCTTCGTATACTGTATATT

     2010      2020      2030      2040      2050      2060      2070      2080      2090      2100
CTTATAGAAATCAGTATCAATTCCTCCCATTTCAATTCAGTTAAGACTTCTGTGATAGATGTTTATAGCAGAGAAGAAATGTCTCATCAATAGGAAAACT
GAATATCTTTAGTCATAGTTAAGGAGGGTAAAGTTAAGTCAATTCTGAAGACACTATCTACAAATATCGTCTCTTCTTTACAGAGTAGTTATCCTTTTGA

     2110      2120      2130      2140      2150      2160      2170      2180      2190      2200
ATCAGATAAAGTTTAGGAGATAGGAAGAAGGACTGTGTGTAGTAATGAAAATACCAAGTTGCAACATTACATGTTTACAAAAAAAATCTGTGTTTGTAGT
TAGTCTATTTCAAATCCTCTATCCTTCTTCCTGACACACATCATTACTTTTATGGTTCAACGTTGTAATGTACAAATGTTTTTTTTAGACACAAACATCA

     2210      2220      2230      2240      2250      2260      2270      2280      2290      2300
GTGGAAGTTGGTGACTGTTTTAATCATCATCTAGACTTGTTAAGTAGAAAAATTTTAAAAATTTGCTTATGAAAATATAACCCCCAGAAAGTAACAATGA
CACCTTCAACCACTGACAAAATTAGTAGTAGATCTGAACAATTCATCTTTTTAAAATTTTTAAACGAATACTTTTATATTGGGGGTCTTTCATTGTTACT

     2310      2320      2330      2340      2350      2360      2370      2380      2390      2400
CAAAGTATTATATTTATATATATTATTGTAGAGAATTTGTATATTTTTAAAGATGTCTTAAGATATCTTAATTTTATTTATAAGTTTTGGTGTTTACCTG
GTTTCATAATATAAATATATATAATAACATCTCTTAAACATATAAAAATTTCTACAGAATTCTATAGAATTAAAATAAATATTCAAAACCACAAATGGAC

     2410      2420      2430      2440      2450      2460      2470      2480      2490      2500
TTTTAAAATGATAATGTTGGCATCTGTGATAAACTATCAATGAGGCTCCCATCATGCCATTTTTTGTTCATTTTAATCTTTAAAAAATAAAAATTAGGCA
AAAATTTTACTATTACAACCGTAGACACTATTTGATAGTTACTCCGAGGGTAGTACGGTAAAAAACAAGTAAAATTAGAAATTTTTTATTTTTAATCCGT

     2510      2520      2530
TATTAAAAAAAAAAAAAAAAAAAAAAAAAAAA
ATAATTTTTTTTTTTTTTTTTTTTTTTTTTTT
```

FIG. 2A

mouse CAP-1

```
        10        20        30        40        50        60        70        80        90       100
ATTCGGCACATGGGATCGAGGGACCATGCCGTTCCAGGTTCAAGGATAAAACCCATTGGGCCATAGTGCCGTCATATTCCACCTTCAGTGCCTTCCTCCA
TAAGCCGTGTACCCTAGCTCCCTGGTACGGCAAGGTCCAAGTTCCTATTTTGGGTAACCCGGTATCACGGCAGTATAAGGTGGAAGTCACGGAAGGAGGT

       110       120       130       140       150       160       170       180       190       200
CAATTGGGATTCACCCCTGCTGAAAAGCGCACGCTGACAGCAAGGGAACAAAAAACTATGCTATCACATAGTGCCATGGTGAAGCAAAGGAAACAGCAAG
GTTAACCCTAAGTGGGGACGACTTTTCGCGTGCGACTGTCGTTCCCTTGTTTTTTGATACGATAGTGTATCACGGTACCACTTCGTTTCCTTTGTCGTTC

       210       220       230       240       250       260       270       280       290       300
CATCAGCCATCACGAAGGAAATCCATGGACATGATGTTGACGGCATGGACCTGGGCAAAAAAGTTAGCATCCCCAGAGACATCATGATAGAAGAATTGTC
GTAGTCGGTAGTGCTTCCTTTAGGTACCTGTACTACAACTGCCGTACCTGGACCCGTTTTTTCAATCGTAGGGGTCTCTGTAGTACTATCTTCTTAACAG

       310       320       330       340       350       360       370       380       390       400
CCATTTCAGTAATCGTGGGGCCAGGCTGTTTAAGATGCGTCAAAGAAGATCTGACAAATACACCTTTGAAAATTTCCAGTATGAATCTAGAGCACAAATT
GGTAAAGTCATTAGCACCCCGGTCCGACAAATTCTACGCAGTTTCTTCTAGACTGTTTATGTGGAAACTTTTAAAGGTCATACTTAGATCTCGTGTTTAA

       410       420       430       440       450       460       470       480       490       500
AATCACAATATCGCCATGCAGAATGGGAGAGTTGATGGAAGCAACCTGGAAGGTGGCTCACAGCAAGGCCCCTCAACTCCGCCCAACACCCCCGATCCAC
TTAGTGTTATAGCGGTACGTCTTACCCTCTCAACTACCTTCGTTGGACCTTCCACCGAGTGTCGTTCCGGGGAGTTGAGGCGGGTTGTGGGGGCTAGGTG

       510       520       530       540       550       560       570       580       590       600
GAAGCCCCCCAAATCCAGAGAACATCGCACCAGGATATTCTGGACCACTGAAGGAAATTCCTCCTGAAAGGTTTAACACGACGGCCGTTCCTAAGTACTA
CTTCGGGGGGTTTAGGTCTCTTGTAGCGTGGTCCTATAAGACCTGGTGACTTCCTTTAAGGAGGACTTTCCAAATTGTGCTGCCGGCAAGGATTCATGAT

       610       620       630       640       650       660       670       680       690       700
CCGGTCTCCATGGGAGCAGGCGATTGGCAGCGATCCGGAGCTCCTGGAGGCTTTGTACCCAAAACTTTTCAAGCCTGAAGGAAAAGCAGAACTGCGGGAT
GGCCAGAGGTACCCTCGTCCGCTAACCGTCGCTAGGCCTCGAGGACCTCCGAAACATGGGTTTTGAAAAGTTCGGACTTCCTTTTCGTCTTGACGCCCTA

       710       720       730       740       750       760       770       780       790       800
TACAGGAGCTTTAACAGGGTTGCCACTCCATTTGGAGGTTTTGAAAAAGCATCAAAAATGGTCAAATTCAAAGTTCCAGATTTTGAACTACTGCTGCTGA
ATGTCCTCGAAATTGTCCCAACGGTGAGGTAAACCTCCAAAACTTTTTCGTAGTTTTTACCAGTTTAAGTTTCAAGGTCTAAAACTTGATGACGACGACT

       810       820       830       840       850       860       870       880       890       900
CAGATCCCAGGTTCTTGGCCTTTGCCAATCCTCTTTCGGGCAGACGATGCTTTAACAGGGCGCCAAAGGGGTGGGTATCTGAGAATATCCCCGTCGTGAT
GTCTAGGGTCCAAGAACCGGAAACGGTTAGGAGAAAGCCCGTCTGCTACGAAATTGTCCCGCGGTTTCCCCACCCATAGACTCTTATAGGGGCAGCACTA

       910       920       930       940       950       960       970       980
CACAACTGAGCCTACAGAAGACGCCACTGTACCGGAATCAGATGACCTGTGAGAGGGAAGCTGGGGATGCCACAGGAAGTTC
GTGTTGACTCGGATGTCTTCTGCGGTGACATGGCCTTAGTCTACTGGACACTCTCCCTTCGACCCCTACGGTGTCCTTCAAG
```

FIG. 2B

human CAP-2

CGGTCACAGC AGCTCAGTCC TCCAAAGCTG CTGGACCCCA GGGAGAGCTG ACCACTGCCC GAGCAGCCGG CTGAATCCAC CTCCACAATG CCGCTCTCAG 100

GAACCCCGGC CCCTAATAAG AAGAGGAAAT CCAGCAAGCT GATCATGGAA CTCACTGGAG GTGGACAGGA GAGCTCAGGC TTGAACCTGG GCAAAAAGAT 200

CAGTGTCCCA AGGGATGTGA TGTTGGAGGA ACTGTCGCTG CTTACCAACC GGGGCTCCAA GATGTTCAAA CTGCGGCAGA TGAGGGTGGA GAAGTTTATT 300

TATGAGAACC ACCCTGATGT TTTCTCTGAC AGCTCAATGG ATCACTTCCA GAAGTTCCTT CCAACAGTGG GGGGACAGCT GGGCACAGCT GGTCAGGGAT 400

TCTCATACAG CAAGAGCAAC GGCAGAGGCG GCAGCCAGGC AGGGGGCAGT GGCTCTGCCG GACAGTATGG CTCTGATCAG CAGCACCATC TGGGCTCTGG 500

GTCTGGAGCT GGGGGTACAG GTGGTCCCGC GGGCCAGGCT GGCAGAGGAG GAGCTGCTGG CACACAGGGG GTTGGTGAGA CAGGATCAGG AGACCAGGCA 600

GGCGGAGAAG GAAAACATAT CACTGTGTTC AAGACCTATA TTTCCCCATG GGAGCGAGCC ATGGGGGTTG ACCCCCAGCA AAAAATGGAA CTTGGCATTG 700

ACCTGCTGGC CTATGGGGCC AAAGCTGAAC TTCCCAAATA TAAGTCCTTC AACAGGACGG CAATGCCCTA TGGTGGATAT GAGAAGGCCT CCAAACGCAT 800

GACCTTCCAG ATGCCCAAGT TTGACCTGGG GCCCTTGCTG AGTGAACCCC TGGTCCTCTA CAACCAAAAC CTCTCCAACA GGCCTTCTTT CAATCGAACC 900

CCTATTCCCT GGCTGAGCTC TGGGGAGCCT GTAGACTACA ACGTGGATAT TGGCATCCCC TTGGATGGAG AAACAGAGGA GCTGTGAGGT GTTTCCTCCT 1000

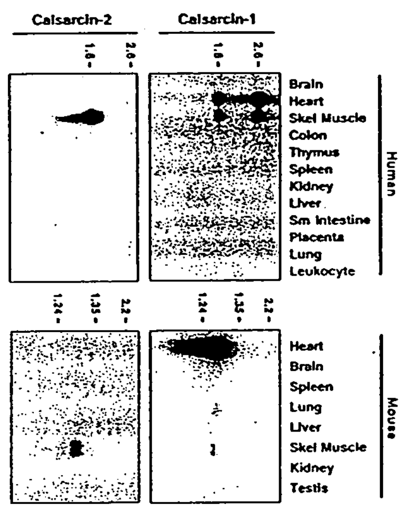
CTGATTTGCA TCATTTCCCC TCTCTGGCTC CAATTTGGAG A

FIG. 2C

mouse CAP-2

100
GCCGGGGAGA GCCGACCACC AACTGAGCAG CTGGTCAGAT CCACCTCCAC CATGCCACGC TCAGGAACCC CGGCCCCTAA CAAGAGGAGG AAGTCAAGCA
200
AACTGATTAT GGAGCTCACT GGAGGTGGCC GGGAGAGCTC AGGCCTGAAC CTGGGCAAGA AGATCAGTGT CCCAAGGGAT GTGATGTTGG AGGAGCTGTC
300
CCTTCTTACC AACCGAGGCT CCAAGATGTT CAAGCTACGG CAGATGCGGG TGGAGAAATT TATCTATGAG AATCACCCCG ATGTTTTCTC TGACAGCTCA
400
ATGGATCACT TCCAGAAGTT TCTTCCCACA GTGGGAGGAC AGCTGGAGAC AGCTGGTCAG GGCTTCTCAT ATGGCAAGGG CAGCAGTGGA GGCCAGGCTG
500
GCAGCAGTGG CTCTGCTGGA CAGTATGGCT CTGACCGTCA TCAGCAGGGC TCTGGGTTTG GAGCTGGGGG TTCAGGTGGT CCTGGGGGCC AGGCTGGTGG
600
AGGAGGAGCT CCTGGCACAG TAGGGCTTGG AGAGCCCGGA TCAGGTGACC AGGCAGGTGG AGATGGAAAA CATGTCACTG TGTTCAAGAC TTATATTTCC
700
CCATGGGATC GGGCCATGGG GGTTGATCCT CAGCAAAAAG TGGAACTTGG CATTGACCTA CTGGCATACG GTGCCAAAGC TGAACTCCCC AAATATAAGT
800
CCTTCAACAG GACAGCAATG CCCTACGGTG GATATGAGAA GGCCTCCAAA CGCATGACCT TCCAGATGCC CAAGTTTGAC CTGGGGCCTC TGCTGAGTGA
900
ACCCCTGGTC CTCTACAACC AGAACCTCTC CAACAGGCCT TCTTTCAATC GAACCCCTAT TCCCTGGTTG AGCTCTGGGG AGCATGTAGA CTACAACGTG
1000
GATGTTGGTA TCCCCTTGGA TGGAGAGACA GAGGAGCTGT GAAGTGCCTC CTCCTGTCAT GTGCATCATT TCCCTTCTCT GGTTCCAATT TGAGAGTGGA
1100
TGCTGGACAG GATGCCCCAA CTGTTAATCC AGTATTCTTG TGGCAATGGA GGGTAAAGGG TGGGGTCCGT TGCCTTTCCA CCCTTCAAGT TCCTGCTCCG
AAGCATCCCT CCTCACCAGC TCAGAGCTCC CATCCTGCTG TACCATATGG AATCTGCTCT TTTATGGAAT TTTCT

FIG. 2D



Calsarcin-2
Calsarcin-1
1.8 -
2.6 -
Brain
Heart
Skel Muscle
Colon
Thymus
Spleen
Kidney
Liver
Sm Intestine
Placenta
Lung
Leukocyte
Human
1.24 -
1.35 -
2.2 -
Heart
Brain
Spleen
Lung
Liver
Skel Muscle
Kidney
Testis
Mouse

FIG. 3

FIG. 4A

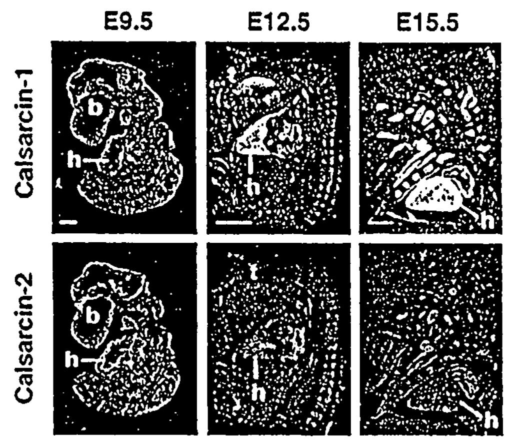


FIG. 4C

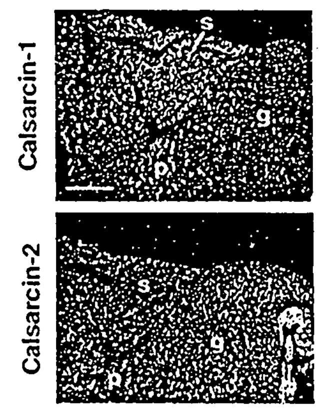


FIG. 4B

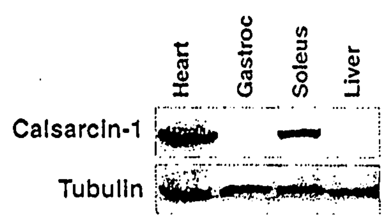


FIG. 4D

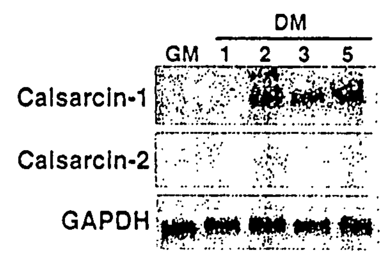


FIG. 4E

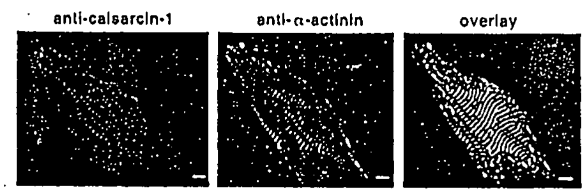

anti-calsarcin-1
anti-α-actinin
overlay

FIG. 5A

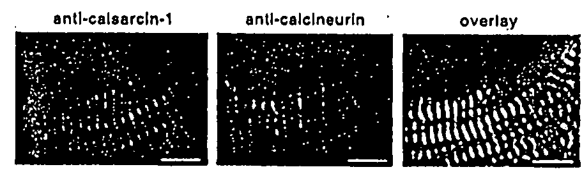

anti-calsarcin-1
anti-calcineurin
overlay

FIG. 5B

FIG. 6A

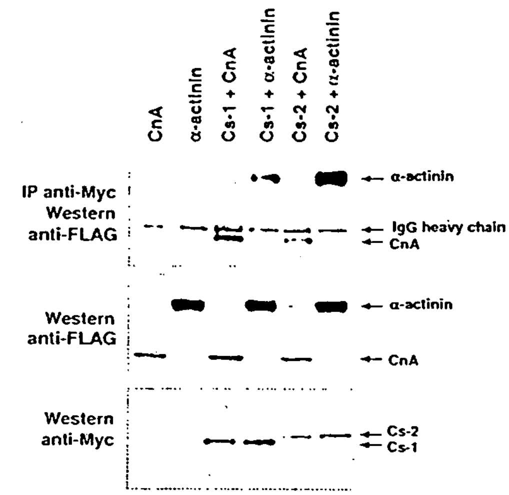


FIG. 6B

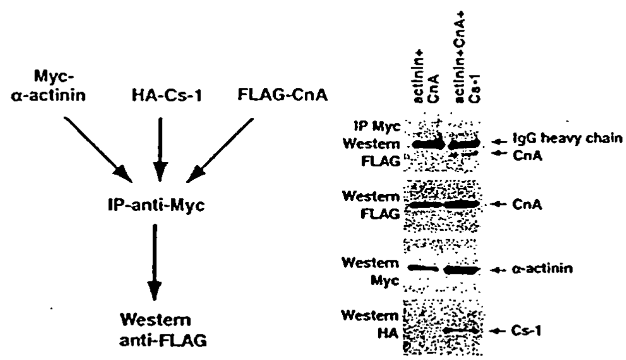
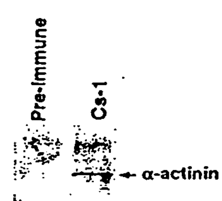


FIG. 6C



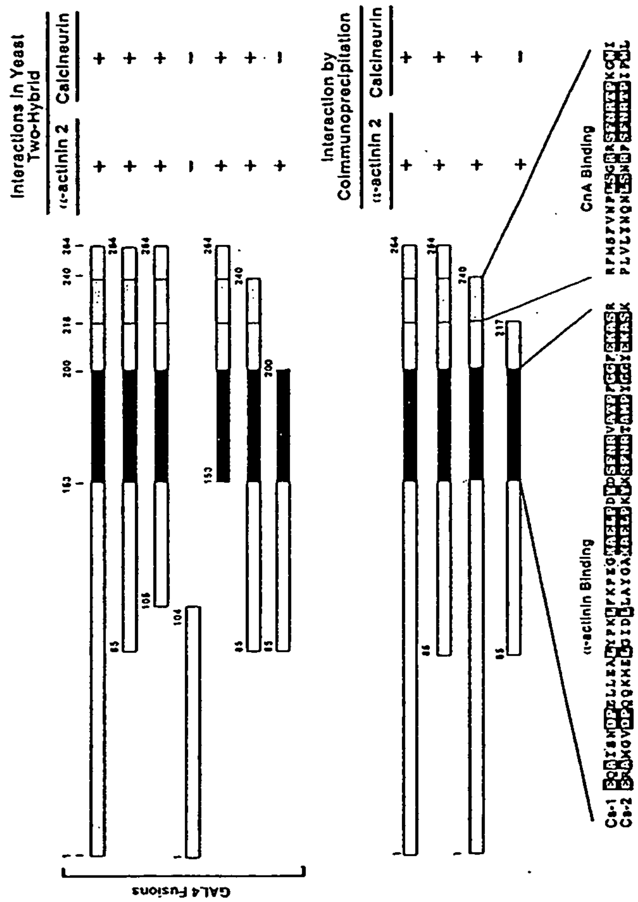
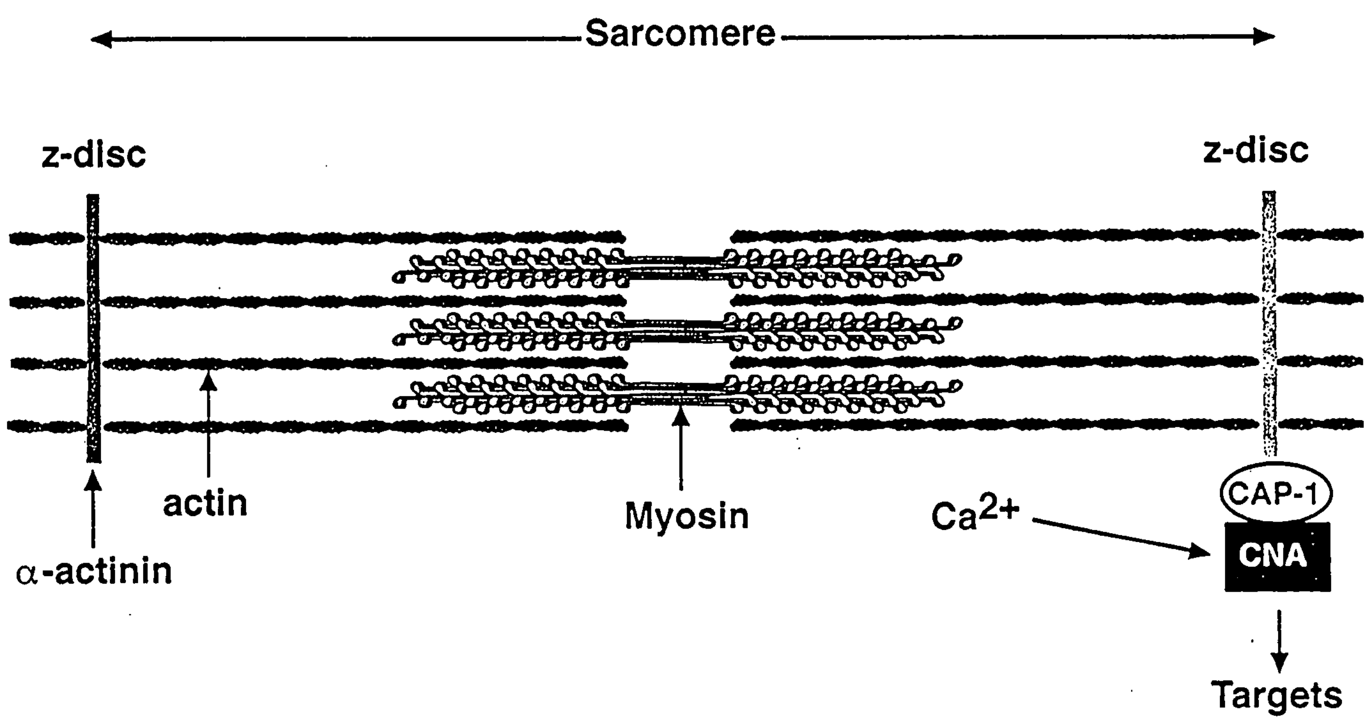

Interactions in Yeast Two-Hybrid
α-actinin 2
Calcineurin
Interaction by Coimmunoprecipitation
α-actinin 2
Calcineurin
GAL4 Fusions
α-actinin Binding
CnA Binding

FIG. 7



Sarcomere
z-disc
z-disc
actin
α-actinin
Myosin
Ca2+
CAP-1
CNA
Targets

FIG. 8

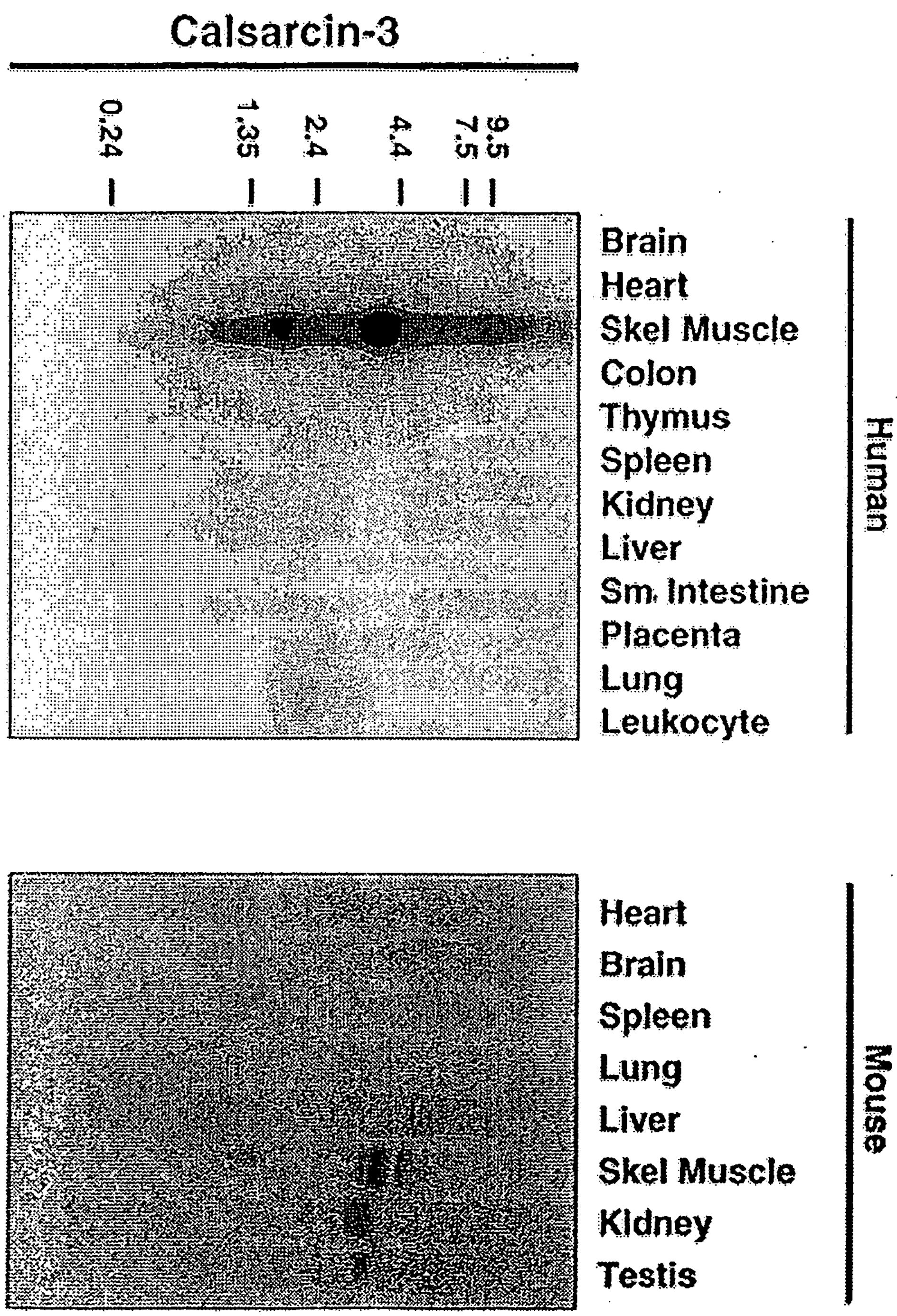

Calsarcin-3
0.24
1.35
2.4
4.4
7.5
9.5
Brain
Heart
Skel Muscle
Colon
Thymus
Spleen
Kidney
Liver
Sm. Intestine
Placenta
Lung
Leukocyte
Human
Heart
Brain
Spleen
Lung
Liver
Skel Muscle
Kidney
Testis
Mouse

FIG. 9

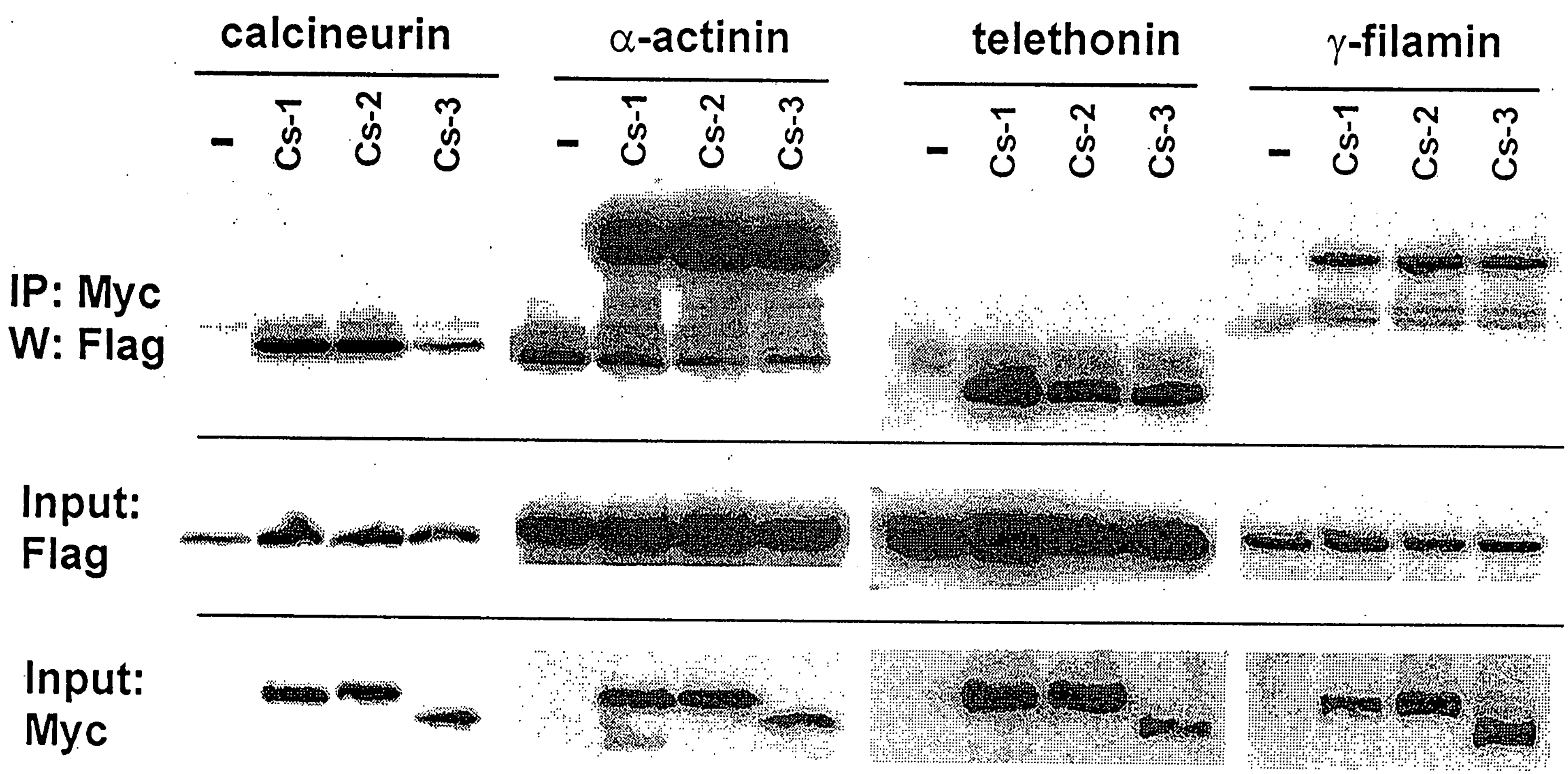


FIG. 10

BEST AVAILABLE COPY

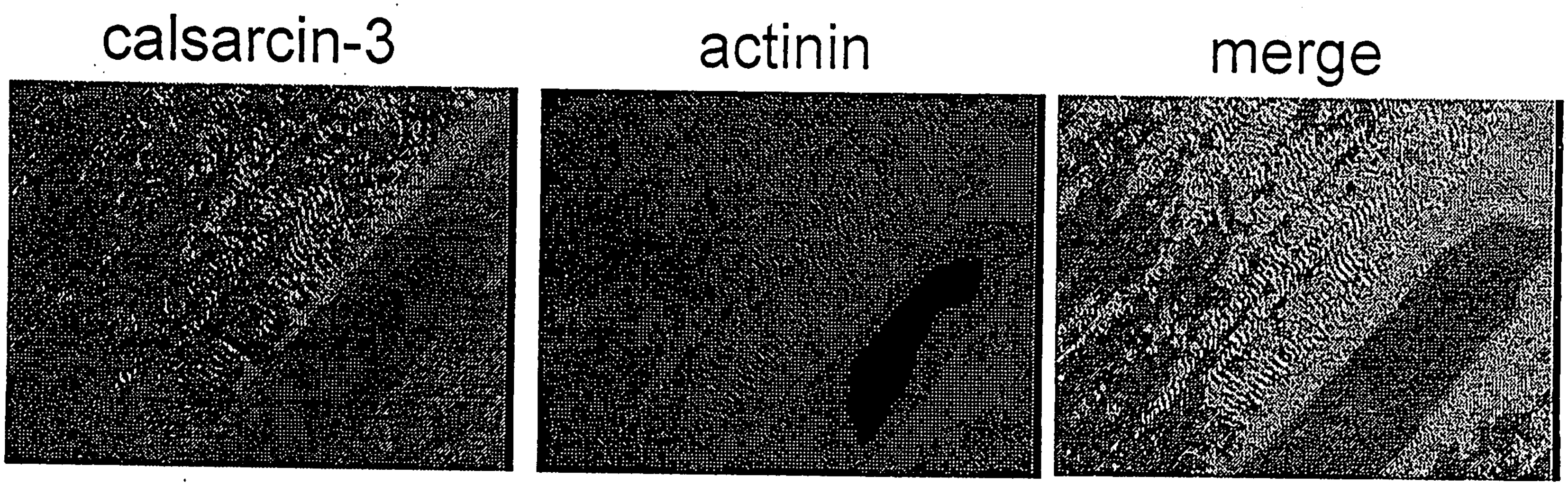
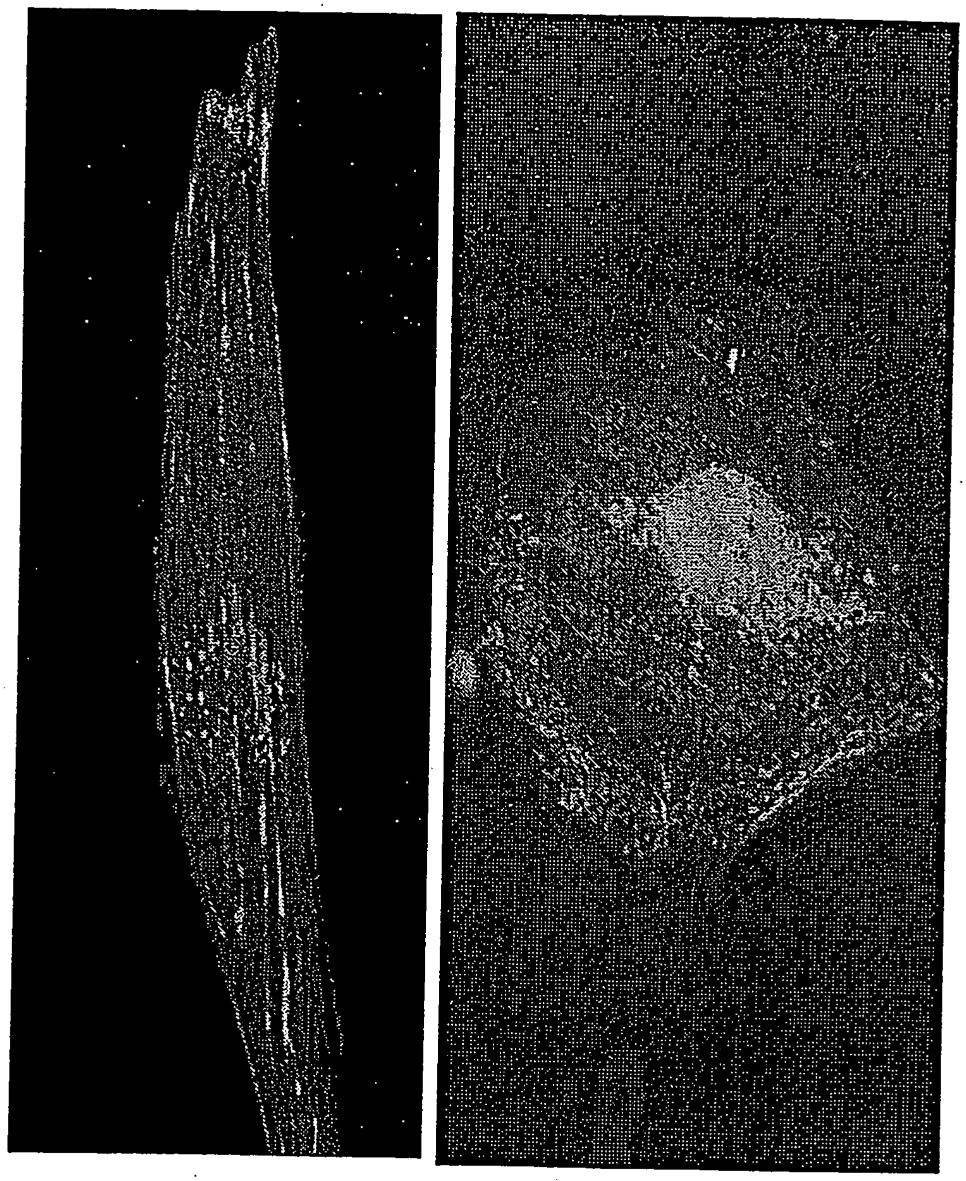


FIG. 11

FIG. 12



BEST AVAILABLE COPY

ClustalW Formatted Alignments

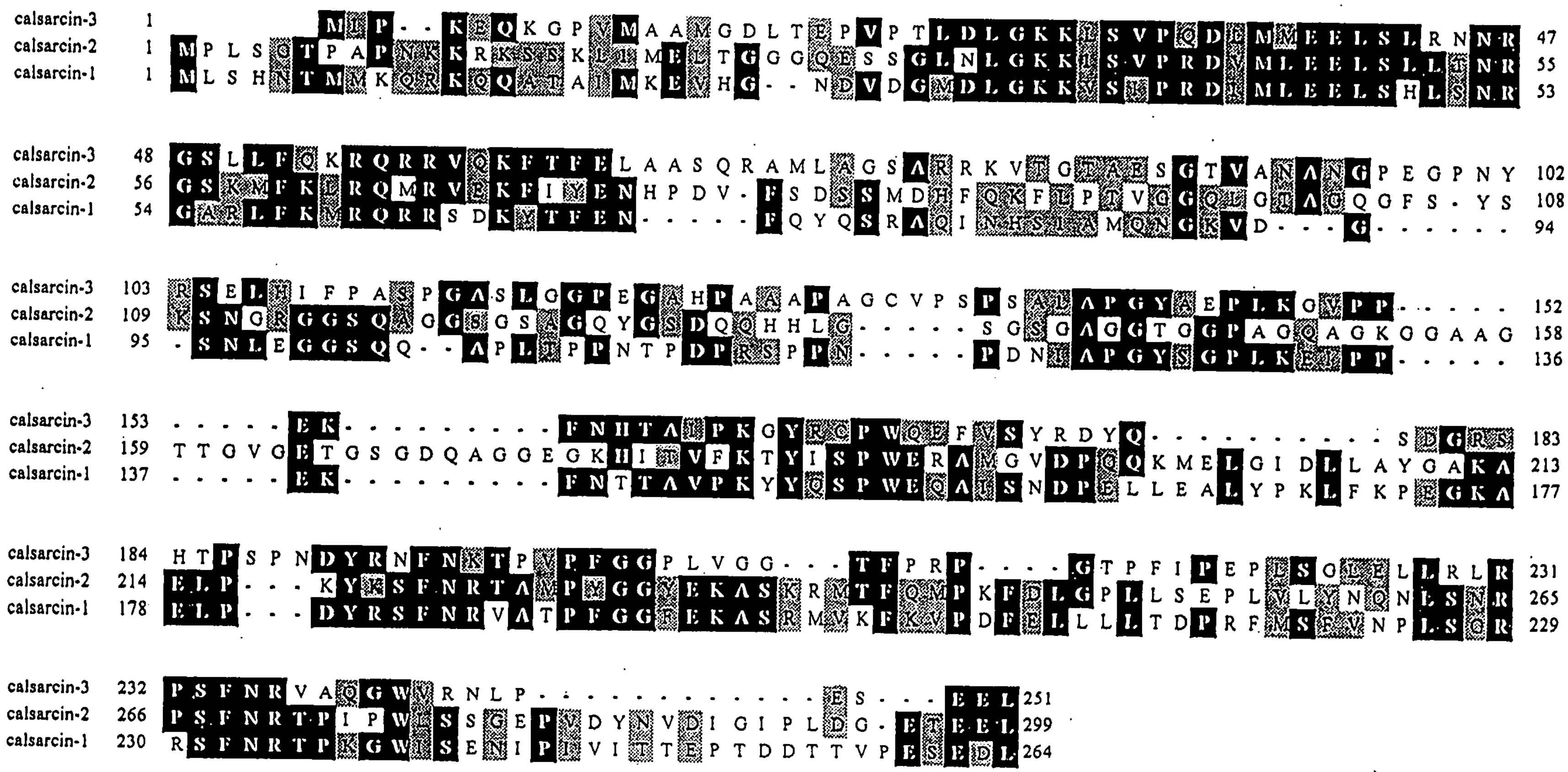


FIG. 13